

SEQUENCE LISTING

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<120> METHODS FOR TREATMENT OF MULTIPLE
 SCLEROSIS USING PEPTIDE ANALOGUES AT POSITION 91
 OF HUMAN MYELIN BASIC PROTEIN

<130> 690068.412C4

<140> US

<141> 2004-04-08

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(516)

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Met Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu	
1 5 10 15	
gcc aca gca agt acc atg gac cat gcc agg cat ggc ttc ctg cca agg	96
Ala Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg	
20 25 30	
cac aga gac acg ggc atc ctt gac tcc atc ggg cgc ttc ttt ggc ggt	144
His Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly	
35 40 45	
gac agg ggt gcg cca aag cgg ggc tct ggc aag gac tca cac cac ccg	192
Asp Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro	
50 55 60	
gca aga act gct cac tat ggc tcc ctg ccc cag aag tca cac ggc cgg	240
Ala Arg Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg	
65 70 75 80	
acc caa gat gaa aac ccc gta gtc cac ttc ttc aag aac att gtg acg	288
Thr Gln Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr	

	85	90	95	
cct cgc aca cca ccc ccg tcg cag gga aag ggg aga gga ctg tcc ctg				336
Pro Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu				
	100	105	110	
agc aga ttt agc tgg ggg gcc gaa ggc cag aga cca gga ttt ggc tac				384
Ser Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr				
	115	120	125	
gga ggc aga gcg tcc gac tat aaa tcg gct cac aag gga ttc aag gga				432
Gly Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly				
	130	135	140	
gtc gat gcc cag ggc acg ctt tcc aaa att ttt aag ctg gga gga aga				480
Val Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg				
	145	150	155	160
gat agt cgc tct gga tca ccc atg gct aga cgc tga				516
Asp Ser Arg Ser Gly Ser Pro Met Ala Arg Arg *				
	165	170		

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<211> 171

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu				
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Ala Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg				
	20	25	30	
His Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly				
	35	40	45	
Asp Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro				
	50	55	60	
Ala Arg Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg				
	65	70	75	80
Thr Gln Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr				
	85	90	95	
Pro Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu				
	100	105	110	
Ser Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr				
	115	120	125	
Gly Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly				
	130	135	140	
Val Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg				
	145	150	155	160
Asp Ser Arg Ser Gly Ser Pro Met Ala Arg Arg				
	165	170		